

Scoring table:	BLOSUM62	Alignments				
Gapext:	0.5					
Searched:	112892 seqs, 41476328 residues					
Total number of hits satisfying chosen parameters:	112892					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing first 45 summaries					
Database :	SwissProt_40:*					
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
1	24.68	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	99.0	478	1 AMP2_HUMAN	P08553 mus musculus
2	23.58	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	94.6	478	1 AMP2_RAT	Q61687 mus musculus
3	23.48	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	94.2	478	1 AMP2_MOUSE	P08199 mesocricetus
4	10.15	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	40.7	421	1 AMP2_YEAST	P46872 strongylococcus
5	4.04	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	16.2	182	1 YD4_CAEEL	Q99mr6 mus musculus
6	3.93	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	15.8	295	1 AMPM_PREFU	P46100 homo sapiens
7	3.75	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	15.0	295	1 AMPM_PRPH	Q01662 saccharomyces
8	3.66	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	14.7	295	1 AMPM_PRAH	Q28181 bos taurus
9	3.47	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	13.9	294	1 AMPM_MEJJA	P91753 lytechinus
10	3.07	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	12.3	291	1 AMPM_ARCFU	Q28092 bos taurus
11	2.71	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	11.8	299	1 AMPM_MFOTH	Q00203 homo sapiens
12	2.71	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	10.9	301	1 AMPM_SULSO	P02369 rat/rattus norvegicus
13	2.25	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	9.0	394	1 P2G4_HUMAN	O2qg80 homo sapiens
14	2.25	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	9.0	394	1 P2G4_MOUSE	P05080 mus musculus
15	1.94	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	7.8	381	1 CDBA_SCHPO	Q09184 schizosaccharomyces pombe
16	1.65	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	6.6	188	1 AMPM_METTE	Q27624 methanobacter
17	1.45	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.8	712	1 NUCL_RAT	P23383 rat/rattus norvegicus
18	1.43	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.7	650	1 NUCL_XENLA	P20397 xenopus laevis
19	1.40	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.6	737	1 PEN_DROME	O61345 drosophila melanogaster
20	1.36	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.5	1997	1 OTOF_HUMAN	Q9esf1 mus musculus
21	1.35	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.4	706	1 NUCL_MOUSE	P19338 homo sapiens
22	1.35	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.4	706	1 NUCL_MOUSE	P03405 mus musculus
23	1.25	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.4	1311	1 ATRX_DROME	Q9eqn5 drosophila melanogaster
24	1.31	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.3	412	1 FBK4_SPOR	P26486 spodoptera frugiperda
25	1.28	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.2	723	1 SSRP_DROME	Q95344 drosophila melanogaster
26	1.26	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.1	767	1 TOP1_CRIGR	Q007050 cricetulus
27	1.24	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	5.0	1612	1 DNMA_PARLI	Q27746 paracentrotus lividus
28	1.21	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	4.9	348	1 CYL2_HUMAN	Q14093 homo sapiens
29	1.20	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	4.8	845	1 NFM_FAT	P12639 rat/rattus norvegicus
30	1.19	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	4.8	517	1 T2FA_HUMAN	P32629 homo sapiens
31	1.19	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	4.8	253	1 AMPL_SYN3	P53579 synechocystis
32	1.18	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	4.8	542	1 TUL1_HUMAN	Q00294 homo sapiens
33	1.18	1 MAGYEEVAASGSIHUNGDLDP XHTILLRPTCKEVYSGDDY	4.8	1359	1 ATRX_CAEEL	Q9u7eo caenorhabditis elegans

RESULT 1						
ID	AMP2_HUMAN	STANDARD;	PRT;	478 AA.		
AC	P50379;	Created)				
DT	01-OCT-1996 (Rel. 34,	Last sequence update)				
DT	01-JUN-2002 (Rel. 41,	Last annotation update)				
DE	Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)					
DE	(Initiation factor 2-associated 67 kDa glycoprotein) (p67) (p67eIF2).					
GN	METAP2 OR MNPEP OR P67eIF2.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TAXID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Brain;					
RX	MEDLINE=93372350; PubMed=7644482;					
RA	Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E.,					
RA	Matthews B.W., Bradshaw R.A.;					
RT	"Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent enzymes."					
RL	PROC. NATL. ACAD. SCI. U.S.A. 92:7714-7718(1995).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Liver;					
RX	MEDLINE=93578556; PubMed=7873610;					
RA	Li J., Chang Y.;					
RA	"Molecular cloning of a human complementary DNA encoding an initiation factor 2-associated protein (p67).";					
RT	RT					
RL	Biochim. Biophys. Acta 1260:333-336(1995).					
RN	[3]					
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 109-478.					
RX	RDLINE=99030697; PubMed=8812888;					
RA	Tiu S., Widom J., Kemp C.W., Crews C.M., Clardy J.;					
RT	"Structure of human methionine aminopeptidase-2 complexed with fumagillin";					
RL	Science 282:1324-1327(1998).					
CC	-!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT PROTEINS.					
CC	CATALYTIC ACTIVITY: Release of N-terminal amino acids.					
CC	preferentially methionine, from peptides and arylamides.					
CC	-!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (BY SIMILARITY).					
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2C.					
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CC	DR: U28607; AAA82930.1;					
DR	EMBL: U13261; AAC64402.1;					
DR	PDB: 1B59; 14-JAN-00.					

THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)						
FEATURES		Location/Qualifiers				
Source	Query	Match	Best Local Similarity	Score	DB 6;	Length
BASE COUNT	957	a	99.88%	1432.8;	DB 6;	2569;
ORIGIN	957	a	99.88%	Pred. No 0;	Mismatches	3;
	Matches 1434;	Conservative	0;	No 0;	Indels	0;
					Gaps	
Qy	1	ATGGCGGCCCTGGAGGAGGTAGCGGCTCCGGAGGCCACCTGAATGGGACTCTGGATCCA	60			
Db	23	ATGGCGGCCCTGGAGGAGGTAGCGGCTCCGGAGGCCACCTGAATGGGACTCTGGATCCA	82			
Qy	61	GACGACGGAAAGAGGAGCTGCTTAACGGTGAAGGAGCCAAAGAAAAAGCAGA	120			
Db	83	GACGACGGAAAGAGGAGCTGGCTCTACGGCTGAGGAGGCCAAAGAAAAAGCAGA	142			
Qy	121	AAGAAAGAGAGAAAGGGCACTGCACCGGGAAACAGGAACCTGATAAGAACATCA	180			
Db	143	AAGAAAGAGAGAAAGGGCAAGGGCTCTGGACCGGGAAACAGGAACCTGATAAGAACATCA	202			
Qy	181	GGAGCCTCACTGGATGAAGTAGCAGAACCTGGGATGGCAGATGGCAACCTGGAAAGAAG	240			
Db	203	GGAGCCTCACTGGATGAAGTAGCAGAACCTGGGATGGCAGACTGGAAAGATAGCA	262			
Qy	241	AGAGATGAAGATGATGAAGATGGGATGGCAGATGGCAACCTGGAAAGAAGAAG	300			
Db	263	AGAGATGAAGATGATGAAGATGGGATGGCAGATGGCAACCTGGAAAGAAGAAG	322			
Qy	301	AAAAGAACAGAACAGAACAGAACAGAACAGAACCTCCCTCAGTTCCATA	360			
Db	323	AAAAGAACAGAACAGAACAGAACAGAACAGAACCTCCCTCAGTTCCATA	382			
Qy	361	TGTGACCTGTATCCATTGGTATTTCCAAAGCACAGAATGGGAATCCCCACACA	420			
Db	383	TGTGACCTGTATCCATTGGTATTTCCAAAGCACAGAATGGGAATCCCCACACA	442			
Qy	421	CAAAGATGGCAACAGCTCTGGAAACTACAAGTGAGAAAAGAACAGATTACATCAG	480			
Db	443	CAGAGTCGGCAACAGCTCTGGAAACTACAAGTGAGAAAAGAACAGATTACATCAG	502			
Qy	481	GCAAGTGAAGAGATTGGATGATTTCGAGAACATGAGAACATGAGAACATGTTAGA	540			
Db	503	GCAAGTGAAGAGATTGGATGATTTCGAGAACATGAGAACATGAGAACATGTTAGA	562			
Qy	541	AATAGCGTAATGAGCTGATCAAGCTGGATGACAATTAGAAATCTGGAAAAAGTTC	600			
Db	563	AATAGCGTAATGAGCTGGATCAAGCTGGATGACAATTAGAAATCTGGAAAAAGTTC	622			
Qy	601	GAAGACTCTTACCCAAGTTAAAGAGAACATGGATTAAATGAGAACATGAAATCTGG	660			
Db	623	GAAGACTCTTACCCAAGTTAAAGAGAACATGGATTAAATGAGAACATGAAATCTGG	682			
Qy	661	ACTGGATGTTCTCTCAATAATTGCTGCTGCCGNTATACTCCCATGCGGTGACACACA	720			
Db	683	ACTGGATGTTCTCTCAATAATTGCTGCTGCCATTATACTCCCATGCGGTGACACACA	742			
Qy	721	GTATTAGCTATGATGACATCTGTAATAGACTTGGAAACATATAAGTGTAGGT	780			
Db	743	GTATTAGCTATGATGACATCTGTAATAGACTTGGAAACATATAAGTGTAGGT	802			
Qy	781	ATGACTGTGCTTTACTGTCACTTTAAATGCCAAATATGATACGTTAAAGCTTA	840			
Db	803	ATGACTGTGCTTTACTGTCACTTTAAATGCCAAATATGATACGTTAAAGCTTA	862			
Qy	841	AAAGATGCTCACTAACACTGGATAAGTGCTGGAAATGTCGTTGTGATCTGATCTG	900			
Db	863	AAAGATGCTCACTAACACTGGATAAGTGCTGGAAATGTCGTTGTGATCTGATCTG	922			

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 21, 2002, 10:31:33 ; Search time 25 Seconds
(without alignments)
793.027 Million cell updates/sec

Title: US-09-943-123-6
Perfect score: 2492
Sequence: 1 MAQEEVAAASGSHLNGDLP.....XHTILLRPTCKEVVSRGDDY 478

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2468	99.0	478	1	AMP2_HUMAN	P50579 homo sapien
2	2358	94.6	478	1	AMP2_RAT	P30062 rattus norvegicus
3	2348	94.2	478	1	AMP2_MOUSE	P00663 mus musculus
4	1015	40.7	421	1	AMP2_YEAST	P38174 saccharomyces cerevisiae
5	404	16.2	182	1	YD43_CAEEL	P50581 caenorhabditis elegans
6	393	15.8	295	1	AMPM_PYRFU	P56218 pyrococcus furiosus
7	375	15.0	295	1	AMPM_PYRHO	P58362 pyrococcus abyssi
8	366	14.7	295	1	AMPM_PRAB	Q9uyt2 pyrococcus abyssi
9	347	13.9	294	1	AMPM_METJUA	Q28418 archaeoglobus fervidus
10	307	12.3	291	1	AMPM_ARCFU	P22624 methanococcus marcusii
11	295	11.8	299	1	AMPM_METTH	P20397 methanobacter wolfei
12	271.5	10.9	301	1	AMPM_SULSO	P95853 sulfolobus solfataricus
13	225.5	9.0	394	1	P2G4_HUMAN	Q9uq80 homo sapien
14	225.5	9.0	394	1	P2G4_MOUSE	P50580 mus musculus
15	194.5	7.8	381	1	CDB4_SCSCO	Q09184 schizosaccharomyces pombe
16	165	6.6	188	1	AMPM_METFE	P22624 methanothermus marcusii
17	145	5.8	712	1	NUCL_MOUSE	P13383 ratnor norvegicus
18	143	5.7	650	1	NUCL_XENLA	P20397 xenopus laevis
19	140.5	5.6	737	1	PEN_DROME	O61345 drosophila melanogaster
20	136.5	5.5	1997	1	OTOF_MOUSE	Q9es11 mus musculus
21	135	5.4	706	1	NUCL_HUMAN	P19338 homo sapien
22	135	5.4	706	1	NUCL_MOUSE	P09405 mus musculus
23	135	5.4	1311	1	ATRX_DROME	Q9gq55 drosophila melanogaster
24	131	5.3	412	1	PKR4_SF0F	Q26496 spodoptera frugiperda
25	128.5	5.2	723	1	SSRP_DROME	Q05344 drosophila melanogaster
26	126	5.1	767	1	TOP1_CRIGR	P07050 cricket paracentrotus lophelia
27	124	5.0	1612	1	DNM1_PARLI	Q27746 paracentrotus lophelia
28	121	4.9	348	1	CYL2_HUMAN	Q14093 homo sapien
29	120.5	4.8	845	1	NFM_RATP	P12839 ratnor norvegicus
30	119.5	4.8	517	1	T2FA_HUMAN	P35269 homo sapien
31	119	4.8	253	1	AMP1_SYN3	P53579 synchocystis sp. PCC6809
32	118.5	4.8	542	1	TU11_HUMAN	Q00294 homo sapien
33	118.5	4.8	1359	1	ATRX_CAEEL	Q9u7eo caenorhabditis elegans

ALIGNMENTS

34	118	4.7	848	1	NFM_MOUSE	P08553 mus musculus
35	118	4.7	2476	1	ATRX_MOUSE	Q61587 mus musculus
36	117	4.7	713	1	NUCL_MESAU	P46872 strongylocentrotus purpuratus
37	116	4.7	699	1	K122_STRPU	Q99m66 mus musculus
38	115.5	4.6	875	1	ARS2_MOUSE	P46100 homo sapiens
39	115.5	4.6	2492	1	ATRX_HUMAN	Q01662 saccharomyces cerevisiae
40	115	4.6	387	1	AMP1_YEAST	Q28181 bos taurus
41	115	4.6	1394	1	CNG4_BOVIN	P91753 lytechinus pictus
42	114.5	4.6	411	1	MP62_LYTP1	P28092 bos taurus
43	114.5	4.6	498	1	CYL2_BOVIN	Q00203 homo sapiens
44	114	4.6	1094	1	A3B1_HUMAN	Q08945 homo sapiens
45	114	4.6	709	1	SSRP_HUMAN	Q98945 homo sapiens

RESULT 1

AMP2_HUMAN	STANDARD;	PRT;	478 AA.
ID	AMP2_HUMAN		
AC	P50579;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)		
DE	Initiation factor 2-associated 67 kDa glycoprotein (P67_EIF2).		
GN	MetAP2 OR MPNEP OR P67_EIF2.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo sapiens		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RC	MEIDLINE=95312350; PubMed=7644482;		
RA	Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E., Matthews B.W., Bradshaw R.A.;		
RA	"Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent enzymes.";		
RT	RT		
RL	RT		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RC	MEIDLINE=95170556; PubMed=7873610;		
RA	Li X., Chang Y.;		
RA	"Molecular cloning of a human complementary DNA encoding an initiation factor 2-associated protein (P67)." ;		
RT	RT		
RL	RT		
RN	[3]		
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 109-478.		
RX	STRUCTURE FROM N.A.		
RA	Liu S., Widom J., Kemp C.W., Creys C.M., Clardy J.; Liu S., Widom J., Kemp C.W., Creys C.M., Clardy J. ;		
RT	"Structure of human methionine aminopeptidase-2 complexed with funagillin."		
RT	Science 282:1324-1327 (1998).		
RL	FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT PROTEINS.		
CC	CC		
CC	PREFERENTIALLY methionine, from peptides and arylamides.		
CC	COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).		
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.		
CC	-!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT PROTEINS.		
CC	CC		
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
DR	DR		
DR	EMBL; U29607; AAA8230.1; -		
DR	U31261; AAC63402.1; -		
DR	PDB; 1B59; 14-JAN-00.		

DR	PDB; 1B6A; 11-JAN-00.	OX	NCBI_TaxID=10116;
DR	MEROPS; M24_002; -.	RN	[1]
DR	GeneW; HGNC_16672; METAP2.	RP	SEQUENCE FROM N.A.
DR	MM; 601870; -.	RC	STRAIN=Reuber H35; TISSUE="Liver";
DR	InterPro; IPR02468; MAP_2.	RX	MEDLINE=93266517; Pubmed=49645;
DR	InterPro; IPR01714; Methionine_Ptase.	RA	Wu S.; Gupta S.; Chatterjee N.; Hileman R.E.; Kinzy T.G.;
DR	Pfam; PF00557; Peptidase_M24.	RA	Denslow N.D.; Merrick W.C.; Chakrabarti D.; Osterman J.C.; Gupta N.K.;
DR	PRINTS; PR00599; MAPPTIDASE_2.	RT	"Cloning and characterization of complementary DNA encoding the eukaryotic initiation factor 2-associated 67-kDa protein (p67)."
DR	TIGRFAMS; TIGR05051; met_pdase_II; 1.	RL	J. Biol. Chem. 268:10796-10801(1993).
DR	PROSITE; PS01202; MAP_2; 1.	RN	[2]
KW	Hydrolase; Aminopeptidase.	RP	REVISONS TO C-TERMINUS.
FT	DOMAIN; 36 46 ARG/LYS-RICH (BASIC).	RX	MEDLINE=937250; Pubmed=7644482;
FT	DOMAIN; 98 93 ASP/GLU-RICH (ACIDIC).	RA	Arfin S.M.; Kendall R.L.; Hall L.; Weaver L.H.; Stewart A.E.;
FT	DOMAIN; 98 106 POLY-LYS.	RA	Matthews B.W.; Braishaw R.A.;
FT	ACT-SITE 231 231 COBALT 2 (BY SIMILARITY).	RT	"Eukaryotic methionine aminopeptidases: two classes of cobalt-dependent enzymes."
FT	METAL 251 251 COBALT 1 AND 2 (BY SIMILARITY).	RT	Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).
FT	METAL 262 262 COBALT 1 (BY SIMILARITY).	RL	CC -1 - FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT PROTEINS.
FT	METAL 331 331 COBALT 1 (BY SIMILARITY).	CC	CC -1 - FUNCTION: PROTECTS EIF-2 ALPHA-SUBUNIT FROM INHIBITORY PHOSPHORYLATION BY EIF-2 KINASES. PLAYS A CRITICAL ROLE IN THE REGULATION OF PROTEIN SYNTHESIS. IT ALSO INTERACTS WITH THE EIF-2 GAMMA-SUBUNIT.
FT	METAL 364 364 COBALT 1 (BY SIMILARITY).	CC	CC -1 - CATALYTIC ACTIVITY: Release of N-terminal amino acids, preferentially methionine, from peptides and arylamides.
FT	METAL 459 459 COBALT 1 AND 2 (BY SIMILARITY).	CC	CC -1 - COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).
SQ	SEQUENCE 478 AA: 52891 MW: 57884BB83E18F9A CRC64; 0;	CC	CC -1 - PTM: CONTAINS 12 O-LINKED GLCNAC.
CC	CC -1 - SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.	CC	CC -1 - SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/	CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
DR	EMBL; L10652; AAA41111.1; -.	DR	DR EMBL; L10652; AAA41111.1; -.
DR	PTR; A46702; A46702.	DR	DR PTR; A46702; A46702.
DR	HSSP; P50579; 1B6A.	DR	DR HSSP; P50579; 1B6A.
DR	MEROPS; M24_002; -.	DR	DR MEROPS; M24_002; -.
DR	InterPro; IPR001714; Metallo_endopeptidase.	DR	DR InterPro; IPR001714; Metallo_endopeptidase.
DR	IPRO02468; MAP_2.	DR	DR IPRO02468; MAP_2.
DR	InterPro; IPR000994; Peptidase_M24.	DR	DR InterPro; IPR000994; Peptidase_M24.
DR	PRINTS; PR00599; MAPPTIDASE.	DR	DR PRINTS; PR00599; MAPPTIDASE.
DR	TIGRFAMS; TIGR0501; met_pdase_II; 1.	DR	DR TIGRFAMS; TIGR0501; met_pdase_II; 1.
DR	PROSITE; PS01202; MAP_2; 1.	DR	DR PROSITE; PS01202; MAP_2; 1.
KW	Hydrolase; Aminopeptidase; Cobalt_Glycoprotein.	FT	FT DOMAIN 36 46 ARG-LYS-RICH (BASIC).
FT	CYTOLYTIC_XPEPTIDASE; COBALT; Glycoprotein.	FT	FT DOMAIN 82 93 ASP/GLU-RICH ACIDIC.
DB	1 YIQLYDICK1DFGTHISGRMTMIECEKLEDCSRSLKLIKENGLNLAXPTGCSLNCAAXYTPNAGDTT 240	FT	FT DOMAIN 98 106 POLY-LYS.
DB	181 KYVMWSIKPGMTMIECEKLEDCSRSLKLIKENGLNLAXPTGCSLNCAAXYTPNAGDTT 240	FT	FT METAL 251 251 COBALT 2 (BY SIMILARITY).
QY	241 VLIQYDICK1XFGTGHISGRMTMIECEKLEDCSRSLKLIKENGLNLAXPTGCSLNCAAXYTPNAGDTT 240	FT	FT METAL 262 262 COBALT 1 AND 2 (BY SIMILARITY).
DB	241 VLIQYDICK1DFGTHISGRMTMIECEKLEDCSRSLKLIKENGLNLAXPTGCSLNCAAXYTPNAGDTT 240	FT	FT METAL 331 331 COBALT 1 (BY SIMILARITY).
DB	301 GEAOEVMESSYEVEIDGKTYQVKPTRKNGXSIGQYRXAGKTVPIKGGEATRMEEGEV 360	FT	FT METAL 364 364 COBALT 1 (BY SIMILARITY).
DB	301 GEAOEVMESSYEVEIDGKTYQVKPIRNNGHSIGQYRHTAGKTVPIKGGEATRMEEGEV 360	FT	FT METAL 459 459 COBALT 1 AND 2 (BY SIMILARITY).
QY	361 YAIXTFFGSGKGVYHDDMECSHMKNFVDGHVPTLRPLTKHLLVINENFGTLAFCRRWL 420	FT	FT CONFLICT 454 478 LRPTCKEVNSRGDDY -> CAQPKVLSAEMNTKT (IN SQ SEQUENCE 478 AA: 53052 MW; BE1C0E91E0CB3D74 CRC64; REF. 1).
DB	361 YAIXTFFGSGKGVYHDDMECSHMKNFVDGHVPTLRPLTKHLLVINENFGTLAFCRRWL 420	Query Match	Query Match 94.6%; Score 2358; DB 1; Length 478;
QY	421 DRUGESKTYLMALKNLCDLGIVDPXPCKDIKSQSYTAOFXTHTLLRPCKEYVSRGDDY 478	Best Local Similarity	Best Local Similarity 92.5%; Pred. No. 1 6e-147;
DB	421 DRUGESKTYLMALKNLCDLGIVDPXPCKDIKSQSYTAOFXTHTLLRPCKEYVSRGDDY 478	Matches	Matches 442; Conservative 10%; Mismatches 26; Indels 0; Gaps 0;
QY	1 MAGVEEVAASSHNLNDLPPDREGAASTAEAKKKKKKKPSAAGEQEPDKES 60	Qy	1 MAGVEEVAASSHNLNDLPPDREGAASTAEAKKKKKKKPSAAGEQEPDKES 60
DB	1 MAGVDEVAROLERSALEDKERDEDDEGDGDDPDRGTSSTAEEAKKKKKKKGAVSAQOELDKES 60	Db	1 MAGVDEVAROLERSALEDKERDEDDEGDGDDPDRGTSSTAEEAKKKKKKKGAVSAQOELDKES 60
OS	61 GASYDEVAKOLERQLEEVKEKDDDEGDGDDPDRGTSSTAEEAKKKKKKKGAVSAQOELDKES 60	Qy	61 GASYDEVAKOLERQLEEVKEKDDDEGDGDDPDRGTSSTAEEAKKKKKKKGAVSAQOELDKES 60
OC	61 GTSDVEAKOLERQLEEVKEKDDDEGDGDDPDRGTSSTAEEAKKKKKKKGAVSAQOELDKES 120	Db	61 GTSDVEAKOLERQLEEVKEKDDDEGDGDDPDRGTSSTAEEAKKKKKKKGAVSAQOELDKES 120

FEATURES	THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
SOURCE	Location/Qualifiers
1.	.2569
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
BASE COUNT	957 a 468 c 542 g 602 t
ORIGIN	
Query Match	99.7%
Best Local Similarity	99.8%
Matches 1434; Conservative	0; Mismatches 3; Indels 0; Gaps
QY	1 ATGGCGGGCTGGAGGAGTAGCGGCCCTGGACCCACCTGAAATGGGACCTGGATCCA 60
Ddb	23 ATGGCGGGCTGGAGGAGTAGCGGCCCTGGACCCACCTGAAATGGGACCTGGATCCA 82
QY	61 GAGCACAGGGAAAGGACTGGCTCAACGGTGTGAAAGCAGCCAAAGAAAAACAGCA 120
Ddb	83 GAGCACAGGGAAAGGACTGGCTCAACGGTGTGAAAGCAGCCAAAGAAAAACAGCA 142
QY	121 AAGAAGAAAGCAAAAGGCCCTCTGCAGCAGGGAAACAGGAACCTGATAAGATCA 180
Ddb	143 AAGAAGAAAGCAAAAGGCCCTCTGCAGCAGGGAAACAGGAACCTGATAAGATCA 202
QY	181 GGACCCCTCACTGGATGAGTTGCAAGAACAGTGTGAAAGATCAGATTGGAGATAAGAA 240
Ddb	203 GGACCCCTCACTGGATGAGTTGCAAGAACAGTGTGAAAGATCAGATTGGAGATAAGAA 262
QY	241 AGAGATGAAGATGATGAGATGGAGATGGCATGGATGGAGATGGGAAACTGGAAAGAAG 300
Ddb	263 AGAGATGAAGATGATGAGATGGAGATGGCATGGATGGAGATGGGAAACTGGAAAGAAG 322
QY	301 AAAAGAGAAAGAAGGACCAAAAGTCAAAAGACCCCTCAGTCACATA 360
Ddb	323 AAAAGAGAAAGAAGGACCAAAAGTCAAAAGACCCCTCAGTCACATA 382
QY	361 TTGACCTGTATCTTAATGGTCTATTTCACAGGACAGAATGGCAATACCCACCCACA 420
b	383 TTGACCTGTATCTTAATGGTCTATTTCACAGGACAGAATGGCAATACCCACCCACA 442
QY	421 CAAGATGGCGAACACTGCTTGGACACTAACAGTGAAGAAAGCAATTAGATCG 480
b	443 CAAGATGGCGAACACTGCTTGGACACTAACAGTGAAGAAAGCAATTAGATCG 502
QY	481 GCAAGTGAAGATTTGGATGATTTGGAGAGCTCGAGAGCACATCGACAAGTTAGA 540
b	503 GCAAGTGAAGATTTGGATGATTTGGAGAGCTCGAGAGCACATCGACAAGTTAGA 562
QY	541 AAATAGTAAATGAGCTGGATCAAATGGGATGACAATGATAAACTGTAAAAGTG 600
b	563 AAATAGTAAATGAGCTGGATCAAATGGGATGACAATGATAAACTGTAAAAGTG 622
QY	601 GAAGACTGTTCACGCCAAGTTAAATGGAGATGGTAATGGAGCTGGCATTCCT 660
b	623 GAAGACTGTTCACGCCAAGTTAAATGGAGATGGTAATGGAGCTGGCATTCCT 682
QY	661 ACTGGATGTCTCTCAATTAATTGTCCTGCCGCTATACTCCCAATGCCGTGACACAAACA 720
b	683 ACTGGATGTCTCTCAATTAATTGTCCTGCCGCTATACTCCCAATGCCGTGACACAAACA 742
QY	721 GTATTACAGTATGAGCTCTGTAAGATTGACTCTGTAATGAGCTTAAATGAGCTTAAAGCTGTA 780
b	743 GTATTACAGTATGAGCTCTGTAAGATTGACTCTGTAATGAGCTTAAAGCTGTA 802
QY	781 ATTGACTGTGCTTTACTGTCACCTTAAATCCCAAATGAGCTTAAAGCTGTA 840
b	803 ATTGACTGTGCTTTACTGTCACCTTAAATCCCAAATGAGCTTAAAGCTGTA 862
QY	841 AAAGATGCTACTACACTGGAAATAAGTGTGCTGGAAATGACTTGTGCTGATGTT 900
b	863 AAAGATGCTACTACACTGGAAATAAGTGTGCTGGAAATGACTTGTGCTGATGTT 922
	SETGAGGCCATCCAAGAAGGTTATGGAGCTCTGAGAATAGATGGAAAGACAT 960

